

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.rni.

[Go Back to previous page](#)

GenCore version 6.3
Copyright (c) 1993 - 2009 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 22:10:23 ; Search time 1097 Seconds
(without alignments)
5968.836 Million cell updates/sec

Title: US-10-573-229A-1

Perfect score: 920

Sequence: 1 tctgttagaggggaatggctg.....acccccaagaaacttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9875436 seqs, 3558593875 residues

Total number of hits satisfying chosen parameters: 19750872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /ABSS/Data/CRF/ptodata/1/ina/1_COMB.seq:*

2: /ABSS/Data/CRF/ptodata/1/ina/5_COMB.seq:*

3: /ABSS/Data/CRF/ptodata/1/ina/6A_COMB.seq:*

4: /ABSS/Data/CRF/ptodata/1/ina/6B_COMB.seq:*

5: /ABSS/Data/CRF/ptodata/1/ina/7A_COMB.seq:*

6: /ABSS/Data/CRF/ptodata/1/ina/7B_COMB.seq:*

7: /ABSS/Data/CRF/ptodata/1/ina/7C_COMB.seq:*

8: /ABSS/Data/CRF/ptodata/1/ina/7D_COMB.seq:*

9: /ABSS/Data/CRF/ptodata/1/ina/HA_COMB.seq:*

10: /ABSS/Data/CRF/ptodata/1/ina/HB_COMB.seq:*

11: /ABSS/Data/CRF/ptodata/1/ina/PCTUS_COMB.seq:*

12: /ABSS/Data/CRF/ptodata/1/ina/PP_COMB.seq:*

13: /ABSS/Data/CRF/ptodata/1/ina/RE_COMB.seq:*

14: /ABSS/Data/CRF/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	322.2	35.0	650	9	US-09-925-065A-602935	Sequence 602935,
2	309.8	33.7	501	9	US-09-925-065A-602938	Sequence 602938,
3	149.6	16.3	485	9	US-09-925-065A-425353	Sequence 425353,
4	122.6	13.3	561	3	US-09-573-080A-108	Sequence 108, App
5	122.6	13.3	561	5	US-09-854-867-108	Sequence 108, App
6	121.2	13.2	541	3	US-09-573-080A-107	Sequence 107, App
7	121.2	13.2	541	5	US-09-854-867-107	Sequence 107, App
c 8	119.6	13.0	493	9	US-09-925-065A-176178	Sequence 176178,
c 9	119.6	13.0	504	10	US-10-301-480C-643499	Sequence 643499,
c 10	109.6	11.9	590	9	US-09-925-065A-73587	Sequence 73587, A
c 11	109.6	11.9	590	9	US-09-925-065A-73588	Sequence 73588, A
c 12	109.6	11.9	590	10	US-10-301-480C-550895	Sequence 550895,
c 13	109.6	11.9	590	10	US-10-301-480C-550896	Sequence 550896,
14	104.8	11.4	737	7	US-10-105-299-6677	Sequence 6677, Ap
15	104.8	11.4	797	7	US-10-105-299-234	Sequence 234, App
c 16	104.8	11.4	137000	3	US-10-172-911-11	Sequence 11, Appl
c 17	98.4	10.7	84105	6	US-10-741-601-5637	Sequence 5637, Ap
c 18	98	10.7	55927	3	US-09-949-016-15017	Sequence 15017, A
c 19	97.8	10.6	9245	3	US-09-949-016-13349	Sequence 13349, A
c 20	97.8	10.6	9245	3	US-09-949-016-13350	Sequence 13350, A
21	93	10.1	948	10	US-10-301-480C-92013	Sequence 92013, A
c 22	91.8	10.0	143550	3	US-09-949-016-14143	Sequence 14143, A
23	91.2	9.9	992	10	US-10-301-480C-220057	Sequence 220057,
24	90.8	9.9	76118	3	US-09-949-016-15593	Sequence 15593, A
25	90.4	9.8	806	10	US-10-301-480C-325534	Sequence 325534,
26	90.2	9.8	564	9	US-09-925-065A-236350	Sequence 236350,
27	90.2	9.8	574	10	US-10-301-480C-695058	Sequence 695058,
28	89.4	9.7	589	10	US-10-301-480C-427272	Sequence 427272,
29	89.4	9.7	589	10	US-10-301-480C-427274	Sequence 427274,
30	89.4	9.7	589	10	US-10-301-480C-605967	Sequence 605967,
31	89.4	9.7	592	9	US-09-925-065A-134131	Sequence 134131,
32	89	9.7	589	10	US-10-301-480C-427273	Sequence 427273,
33	88.4	9.6	987	10	US-10-301-480C-932619	Sequence 932619,
c 34	86.6	9.4	660	10	US-10-301-480C-296865	Sequence 296865,
c 35	85.4	9.3	870	10	US-10-301-480C-296866	Sequence 296866,
36	85.2	9.3	463	9	US-09-925-065A-594086	Sequence 594086,
37	85.2	9.3	575	9	US-09-925-065A-333372	Sequence 333372,
38	85.2	9.3	577	10	US-10-301-480C-783034	Sequence 783034,
39	85.2	9.3	986	10	US-10-301-480C-163837	Sequence 163837,
40	85.2	9.3	987	10	US-10-301-480C-950354	Sequence 950354,
41	85.2	9.3	987	10	US-10-301-480C-950355	Sequence 950355,
42	84.8	9.2	915	8	US-10-098-754-678	Sequence 678, App
43	84.2	9.2	997	10	US-10-301-480C-326425	Sequence 326425,
44	84.2	9.2	55927	3	US-09-949-016-15017	Sequence 15017, A
c 45	84	9.1	601	3	US-09-949-016-178228	Sequence 178228,

ALIGNMENTS

RESULT 1

US-09-925-065A-602935
; Sequence 602935, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602935
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602935

Query Match 35.0%; Score 322.2; DB 9; Length 650;
Best Local Similarity 95.4%; Pred. No. 1.2e-93;
Matches 354; Conservative 0; Mismatches 13; Indels 4; Gaps 2;

Qy	373	GCTGGGCAGTGAGAACATCACCCACTTCCCCAGAACCTTTTACGTGGAGTGAAAAC	432
Db	1	GCTGGGCAGTGAGAACATCACCCACTTCCCCAGAACCTTTTACGTGGAGTGAAAAC	60
Qy	433	TTAAAGGGCTGTCCAGCTAACCTCCAACCTCCAGATCCATGCCAATTCTCTGCTTC	492
Db	61	TTAAAGGGCTGTCCAGCTAACCTCCAACCTCCAGATCCATGCCAATTCTCTGCTTC	120
Qy	493	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGTAAACCCCTCCCTG	552
Db	121	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGTAAACCCCTCCCTG	180
Qy	553	CCCCAGGCCAACAGAAGGATTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	612
Db	181	CCCCAGGCCAACAGAAGGATTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	240
Qy	613	ACCCCTGGAGAGGGAGGGAGGGAAATCTCGAGGACAGGGTTATGCAACAAACACAAGGGA	672
Db	241	ACCCCTGGAGAGGGAGGGAGGGAAATCTCGAGGACAGGGTTATGCAACAAACACAAGGGA	300
Qy	673	AGTACCTGCTGGGTTCTGGGGTTGGGAAGGGAAAATCCCTACTGCCCAAGAGCCAGCC	732

Db	301	AGTACCTGCTGG---TTCTGGGTTGGGAGGAAGATCCCTACTG-CCCAAGAGGCCAGCA	356
Qy	733	CCGAACCCAAG 743	
Db	357	CAGACACAAAGG 367	

RESULT 2

US-09-925-065A-602938

; Sequence 602938, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602938
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602938

Query Match 33.7%; Score 309.8; DB 9; Length 501;
Best Local Similarity 94.5%; Pred. No. 1.1e-89;
Matches 343; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

Qy	381	ACTGAGAACATCACCCACTTCCCAGAACCTTTACGTGGAGTGTAAAACTTAAGGG	440
Db	1	ACTGAGAACATCACCCACTTCCCAGAGCCTTTACATGGAGTGTAAAACTTAAGGG	60
Qy	441	GCTGTCCAGCTAACCTCAACCTCCAGATCCCAGATGCCATTCTGCTTCTGCAAAG	500
Db	61	GCTGTCCAGCTAACCTCAACCTCCAGATCCCAGATGCCAGTTCTGCTTCTGCAAAG	120
Qy	501	GACTTCAAGTGAAGACATCTGCAGCTGTGAACGGGGTAAACCCCTCCCTGCCAGGC	560
Db	121	GACTTCAAGTGAAGACATCTGCAGCTGTGAACGGGGTAAACCCCTCCCTGCCAGGC	180
Qy	561	CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAACATCGAGAGACCTCTAACCTGGG	620
Db	181	CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAACATCGAAACACACAAGGGAAAGTACCTG	240
Qy	621	AGAGGAGGGAGGGAAATCTCGAGGACCAGGGTTATGCAACAAACACAAGGGAAAGTACCTG	680

```

Db      241 AGAGGAGGGAGGGAAATCTCGAGGCCAGGGTTATGCAACACACAAGGGAAAGTACCTG 300
Qy      681 CTGGGTTCTGGGGGTGAGGAAATCCCTACTGCCCAAGAGCCAGCCCCGACCC 740
Db      301 CTGG--TTCTGGGGTCAGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCACAGACACA 357
Qy      741 AAG 743
Db      358 AGG 360

```

RESULT 3

US-09-925-065A-425353

```

; Sequence 425353, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425353
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-425353

```

```

Query Match      16.3%;  Score 149.6;  DB 9;  Length 485;
Best Local Similarity  91.0%;  Pred. No. 1.5e-37;
Matches 193;  Conservative  0;  Mismatches  14;  Indels  5;  Gaps  3;

```

```

Qy      532 ACGGGGTAAAACCTCCCTGCCCAAGGCCCAAGCAAGGATTCCTAGGGGGAGGA 591
Db      1 ACGGGGTAAAACCTCCCTGCCCAAGGCCCAAGCAAGGATTCCTAGGGGGAGGA 60
Qy      592 GGTAGAATCGAGAGACCTCTAACCTGGGAGAGGAGGGAGGGAAATCTCGAGGACAGG 651
Db      61 GGTAGAATCGAGAGACCTCTAA-CCTGGGAGAGGAGGGAGGGAAATCTCGAGGACAGG 119
Qy      652 GTTATGCAACACACAAGGGAAAGTACCTGCTGGTTCTGGGGTTGGGAAGGAAATCC 711
Db      120 GTTATGCAACACACAAGGGAAAGTACCTGCTGG--TTCTGGGTTGGGAGGAAGATCC 176

```


Db	321	ACAGCCATGTGAGTGAGCATCTTGGAAAGCAGATCCTCCAGCCCCAGTCAGCCCTTCAGA 380
Qy	168	TGGCTGCAGCCACAGCCAAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAAC 227
Db	381	TGACTGCAGCCCCAGCTAACATCTGACTGCAACCTCATGAGAGACCTGAGCCAGAAC 440
Qy	228	CCCTGGCTAAATTGTCCTTGATTCTAACCCACAGAAATTGTGTAAGA 276
Db	441	ACCCAGCTAACGTCCTAACATTCTGACCCACAGAAACTGTGAGAGA 489

RESULT 5

US-09-854-867-108

; Sequence 108, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(561)
; OTHER INFORMATION: mlt1fl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)..(62)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (165)..(165)
; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-108

Query Match 13.3%; Score 122.6; DB 5; Length 561;
Best Local Similarity 69.6%; Pred. No. 1e-28;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy	2	CTGTAGAGGGAAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
Db	201	CTCTGGGGAAAGCCAGCTGCCATGTGTCATGAGGACACTCAAGCAGCCCCGTGGAGAGGCC 260
Qy	62	ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGT----- 114
Db	261	ATGTGCAAGGAAGTGGAGGCCCTCTGCCAACAGCCAGCAAGGAAGTGGAGGCCCTGCCA 320
Qy	115	-----TGAGACTGAGCCACTTGGAGACTGATCTGGAGCACCGAGTCAGCCCTTAGC 167

Db	321	ACAGCCATGTGAGTGGCATCTTGGAAAGCAGATCCTCCAGCCCCAGTCAGCCTTCAGA 380
Qy	168	TGGCTGCAGCCACAGCAACAAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAAC 227
Db	381	TGACTGCAGCCCCAGCTAACATCTGACTGCAACCTCATGAGAGACCTGAGCCAGAAC 440
Qy	228	CCCTGGCTAAATTGTCCTTGATTCTAACCCACAGAAATTGTGTAAGA 276
Db	441	ACCCAGCTAACGCTGCTCTAAATTCTGACCCACAGAAACTGTGAGAGA 489

RESULT 6

US-09-573-080A-107

; Sequence 107, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(541)
; OTHER INFORMATION: mlt1f
; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-__
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: ____-__-__
; DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-107

Query Match 13.2%; Score 121.2; DB 3; Length 541;
Best Local Similarity 68.8%; Pred. No. 2.8e-28;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

Qy	2	CTGTAGAGGGATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 61
Db	197	CTCTGGGGAAAGCCAGCTGCCATCTGAAGACACTCAAGCAGCTA-TGGAGAAGTCC 255

Qy	62	ACTTGGTGAGAAACCAGATGCCT-CTGCCAACACCCTGCACTAACCTGCTGGGCTGAGAC	120
		:	
Db	256	ACGTGGSAAAGGAAGTGGCTCTCTGCCAACAGCCAGCTTCGACYTGCGAGCCATGTGAG	315
Qy	121	TGAGGCCACTTGGAAAGCTGATCTGGAGCACCGAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
		:	
Db	316	TGAGGCCATCTGGAAAGGGATCCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC	375
Qy	181	AGCCAACAACAAGACTGCAACCTCTGGGGGATCCTGAGCCAGAACCCCCGGCTAAATT	240
Db	376	GGCTGACATCTTGAATGCCAACCTCATGAGAGACCCCTGAGCCAGAACCTACCAGCTAAGCT	435
Qy	241	GCTCCTTGTATTCTAACCCACAGAAAATTGTGTAAGA	276
		:	
Db	436	GCTCCTTGTATTCTGACCCACAGAAAATGTTGAGATA	471

RESULT

US-09-854-867-107
; Sequence 107, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(541)
; OTHER INFORMATION: mlt1f
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (179)..(179)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-107

Query Match 13.2%; Score 121.2; DB 5; Length 541;
Best Local Similarity 68.8%; Pred. No. 2.8e-28;
Matches 190: Conservative 3: Mismatches 81: Indels 2: Gaps 2:

Qy	62	ACTGGTGAGAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGCTGAGAC	120
		:	
Db	256	ACGTGGSAAAGGAAGTCTGAGGCTCTGCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG	315

Qy	121	TGAGGCCACTTGGAAAGCTGATCTTGGAGCACAGTCAGGCCCTAGCTGGCTGCAGCCAC	180
Db	316	TGAGGCCATCTTGGAAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC	375
Qy	181	AGCCAACAACAAGACTGCAACCTCTGGGGATCTGAGCCAGAACTCCCTGGCTAAATT	240
Db	376	GGCTGACATCTTGACTGCAACCTCATGAGAGACCCCTGAGCCAGAACTACCCAGCTAAGCT	435
Qy	241	GCTCCTTGATTCTAACCCACAGAAATTGTGTAAGA	276
Db	436	GCTCCTARATTCTGACCCACAGAAACTGTGAGATA	471

RESULT 8

US-09-925-065A-176178/c

; Sequence 176178, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 176178

; LENGTH: 493

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-176178

Query Match 13.0%; Score 119.6; DB 9; Length 493;
 Best Local Similarity 66.7%; Pred. No. 9e-28;
 Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

Qy	2	CTGTAGAGGGAAATGGCTGCTGTCTGGGGTGATGAGCAGCCAGTGGAGAGGTGC	61
Db	419	CTCTGGAGGAAGTCAGCTGCTGTCTGGGGACTCAAAAGCCCTATGAAGAGGTCC	360
Qy	62	ACTTGGTGAACCGATGCC-TCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	359	ATGTGTTAAGGAACTGAGGACTTCTGCCAACAGGCCAGCAATAACTTGCAGGTATGTGAA	300
Qy	121	TGAGGCCACTTGGAAAGCTGATCTTGGAGCACAGTCAGGCCCTAGCTGGCTGCAGCCAC	180
Db	299	TGAGGCCATCTTGGAAAGCAAGTCTCCAACTCCAGACAGCTCTCTAATAACTGTGGCCCC	240

Qy	181	AGCCAACAACAAGACTGCAACCTCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATT	240
Db	239	AGCTGACATCTTGGCTGCAACCCACAGGGGAATCTGAGCCAGCACCACCAAGMTAAGCC	180
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA	276
Db	179	ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA	144

RESULT 9

US-10-301-480C-643499/c

; Sequence 643499, Application US/10301480C

; Patent No. H002220

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827-137

; CURRENT APPLICATION NUMBER: US/10/301,480C

; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 10/215,598

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/311,695

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 989478

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 643499

; LENGTH: 504

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-301-480C-643499

Query Match 13.0%; Score 119.6; DB 10; Length 504;
 Best Local Similarity 66.7%; Pred. No. 9.1e-28;
 Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

Qy	2	CTGTAGAGGGGAATGGCTGCTGTGATGGGGGTGATGAGCAGCCCAGTGGAGAGGTGC	61
Db	430	CTCTGGAGGAAGTCAGCTGCTGTGATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC	371

Qy	62	ACTTGGTGAGAACCGATGCC-TCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	370	ATGTGTTAAGGAAGTCTGAGGACTTCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA	311

Qy	121	TGAGGCCACTTGGAAAGCTGATCTGGAGCACCACTGCAAGCCCTAAGCTGGCTGCAGCCAC	180
Db	310	TGTGCCATCTTGGAAAGCAAGTCTCCAACCTCCAGACAGCTCTAATAACTGTGGCCCC	251

Qy	181	AGCCAACAACAAGACTGCAACCTCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATT	240
Db	250	AGCTGACATCTTGGCTGCAACCCACAGGGGAATCTGAGCCAGCACCACCAAGMTAAGCC	191

Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA	276
Db	190	ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA	155

RESULT 10
US-09-925-065A-73587/c
; Sequence 73587, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73587
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73587

Query Match 11.9%; Score 109.6; DB 9; Length 590;
 Best Local Similarity 63.8%; Pred. No. 1.8e-24;
 Matches 166: Conservative 0; Mismatches 94; Indels 0; Gaps 0

Qy 17 GCTGCTGTCTATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76

Qv 77 GAIGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGGCCATTGGAAAG 136

Db 239 AGGTCTCTGCCAACAAACAGCATTAACATTCCAGGCTTGTGGGTGAGTCCTTGGAAAG 180

Db 179 CAGATCCTCCAGACTCAGTCAGGCCATCAGATGACTGCAGTCCCAGGTGATGCCAAGCT 120

Qy	257	CCACAGAAATTGTGTAAGA	276
Ds	59	CCTACACGAACTCTCTGACA	40

RESULT 11

; Sequence 73588, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73588
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73588

```
Query Match           11.9%;  Score 109.6;  DB 9;  Length 590;
Best Local Similarity 63.8%;  Pred. No. 1.8e-24;
Matches 166;  Conservative 0;  Mismatches 94;  Indels 0;  Gaps 0;
```

Qy 17 GCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76

QY 77 GATGCCTGCCAACCACTGCACTAACCTGCTGGGCTGAGACTGAGGCACTTTGAAAG 136

DB 259 AGGCTCTGCCACACCCAGCATTAACATTCAGGCTTGAGGCTGGGGAG 180
Qy 137 CTGATCTTGGAGCACCGAGTCAGGCCCTTAGCTGGCTGCAGGCCACAGCCAACAAAGACT 196

Db 179 CAGATCCTCCAGACTCAGTCAGCCATCAGATGACTGCAGTCCCAGGTGATGCCAAGCT 120

QY	197	GCAACCTCTGGGGGATCTTGAGCCAGAGTCCCCCTGGCTAAATGCTCTCTGATCTAA	236
Db	119	GCAACCTCAAGAAAGATCTCTGAGCCAGAACCACTCAGCTAAAGTAGCTCTCAGGGTCTG	60

Qy	257	CCCACAGAAATTGTGTAAAGA	27
Db	59	CCTACAGCAACTGTGTGAGA	40

RESULT 12

US-10-301-480C-550895/6

; Sequence 550895, Application US/103014800

Patent No. H002220

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550895
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US 10,301,480C, 550895

```

Query Match           11.9%;  Score 109.6;  DB 10;  Length 590;
Best Local Similarity 63.8%;  Pred. No. 1.8e-24;
Matches 166;  Conservative 0;  Mismatches 94;  Indels 0;  Gaps 0;

Qy      17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGGGTGCACCTGGTGAGAACCC 76
        ||||| | ||||||| ||| | ||||| | | ||||| | | ||||| | | ||||| | | ||||| |
Db      299 GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAAGGTCCACATGGCAAGGAACCTG 240

Qy      77 GATGCCCTCTGCCAACCAACCTGCACTAACCTGCTGGGCTGAGACTGAGCCACTTGGAG 136
        | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| |
Db      239 AGGTCTTCTGCCAACAACCGCATTAACATTCCAGGCTGTGGGTGAGTCCCTTGGAG 180

Qy      137 CTGATCTGGAGCACCAGTCAGGCCCTAGCTGGCTGCAGCCACAGCCAAACAAGACT 196
        | | ||||| | | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| |
Db      179 CAGATCCTCCAGACTCAGTCAGGCCATCAGATGACTGCAGTCCCAGGTGATGCCAACGCT 120

Qy      197 GCAACCTCTGGGGATCCTGAGCCAGAACCTGGCTAAATTGCTCTTGATTCTAA 256
        | | ||||| | | | ||||| | | | ||||| | | | ||||| | | | ||||| | | |
Db      119 GCAACCTCAAGAAAGATCCTGAGCCAGAACACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy      257 CCCACAGAAATTGTGTAAGA 276
        | | ||||| | | | ||||| |
Db      59 CCTACAGCAACTGTGTGAGA 40

```

RESULT 13

US-10-301-480C-550896/9

: Sequence 550896, Application US/10301480C

Patent No. H002220

GENERAL INFORMATION:

APPLICANT: Wang, David G.

1. TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucle

; FILE REFERENCE: 108827-137

; CURRENT APPLICATION NUMBER: US/1

; CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2002-08-09

; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550896
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550896

RESULT 14

US-10-105-299-6677

; Sequence 6677, Application US/1010529

; Patent No. 7368527

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

;

TITLE OF INVENTION:

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,291

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palms

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 667

; LENGTH: 73

; TYPE: DNA

; ORGANISM: *Homo sapiens*

US-10-105-299-667

Query Match 11.4%; Score 104.8; DB 7; Length 737;
Best Local Similarity 68.5%; Pred. No. 7.3e-23;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy	24	TGTATGGGGTGCATGAGCAGCCCAGTGGAGGGTGCAGTGGTGGAGAACCGATGCCT	83
Db	398	TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGGAGAAACTGAAGCC	457
Qy	84	-CTGCCAACCACCTGCACTAACCTGCTGGTCTGAGACTGAGCCACTTGGAAAGCTGATC	142
Db	458	CCTACCAAGAGCCAGCACCAACTTGCAGCTATGTGAATGAGCCATCTAGAAAGTGGGTT	517
Qy	143	TTGGAGCACCGAGTCAGGCCCTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC	202
Db	518	CTCTAGGCCCTAGTCAGGCCCTCATATGACTGCAGCCAGGGCTGATATTGACTACAACC	577
Qy	203	TCCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATTGCTCCTGATTCTAACCCACA	262
Db	578	TCATGAGAGA--CTGAGGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCCTACCAACA	635
Qy	263	GAAATTGTGTAAGA	276
Db	636	GAAGATATGTGAGA	649

RESULT 15

US-10-105-299-234

; Sequence 234, Application US/10105299

; Patent No. 7368527

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

1. TITLE OF INVENTION: REMOVABLE

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/1

; CURRENT FILING DATE: 2002-

NUMBER OF SEQ ID NOS: 15197

Prior Application removed

SOFTWARE: PatentIn Ver. 2.0

1. SECURITY INFORMATION FORM

LENTH: 797

TYPE: DNA

ORGANISM

US-10-105-389-334

00-10-100-200-250

```
Query Match      11.4%;  Score 104.8;  DB 7;  Length 797;
Best Local Similarity  68.5%;  Pred. No. 7.7e-23;
Matches 174;  Conservative  0;  Mismatches  77;  Indels  3;  Gaps  2;
```

Qy 84 -CTGCCAACACCTGCACTAACCTGCTGGGCTGAGACTGAGCCACTTGGAAAGCTGATC 142
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 143 TTGGAGCACCACTAAGCCCTAGCTGGCTGCAGCCACAGCCAACAAGACTGCAACC 202

Ov 203 TCCGGGGATCTGAGCCAGAATCCCTGGCTAAATTGCTCTGATTCTAACCCACA 262

Db 563 TCATGAGAGA--CTGAGCCACAACACCTAGCTAAGAAGCTCCTGAATTCCCTACCAACA 620
Qy 263 GAAATTGTGTAAGA 276
Db 621 GAAACTATGTGAGA 634

Search completed: May 31, 2009, 22:28:46

Job time : 1103 secs

SCOPE 34